

Heps	RIVGGRDTSL	GRWPWQVSL.	....RYDG.A	HLCGGSLLSG	DWVLTAACHF	PE....RNRV
Tadg15	RVVGGTDADE	GEWPWQVSL.	....HALGQG	HICGASLISP	NWLVSAAHCY	IDDRGFRYSD
Scce	KIIDGAPCAR	GSHPWQVAL.	....LSGNQL	H.CGGVLVNE	RWVLTAACH.	.....K
Try	KIVGGYNCEE	NSVPYQVSL.	....NSGYHF	..CGGSLINE	QWVVSAGHC.	.....Y
Chymb	RIVNGEDAVP	GSWPWQVSL.	....QDKTGF	HFCGGSLISE	DQVVTAACH.	.....GV
Fac7	RIVGGKVC PK	GECPWQVLL.	....LVNG.A	QLCGGTLINT	IWVVSAAACHF	DKIKNWRNLI
Tpa	RIKGGLFADI	ASHPWQAAIF	AKHRRSPGER	FLCGGILISS	CWILSAAACHF	QERFPPHHL.
						*
Heps	LSRWRVFAGA	VAQASPHGLQ	LGVQAVVYHG	GYPFRDPNS	EENSNDIALV	HLSS.PLPLT
Tadg15	PTWETAFLHL	HDQSQRSAPG	VQERRLKRII	SHPPFNDFTF	D...YDIALL	ELEK.FAEYS
Scce	MNEYTVHLGS	DTLG..DR.R	AQRIKASKSF	RHPGYSTQT.	..HVNDLMLV	KLNS.QARLS
Try	KSRIQVRLGE	HNIEVLEG.N	EQFINAAKII	RHPQYDRKT.	..LNNDIMLI	KLSS.RAVIN
Chymb	RTSDVVVAGE	FDQGSDEE.N	IQVLKIAKVF	KNPKFSILT.	..VNNDITLL	KLAT.PARFS
Fac7	....AVLGE	HDLSEHDGDE	QSRRVAQVII	P....STYVP	GTTNHDIALL	RLHQ.PVULT
Tpa	....TVILGR	.TYRVVPGEE	EQKFEVEKYI	VHKEFDDDTY	D...NDIALL	QLKSDSSRCA
Heps	EYIQPVCLPA	...AGQALVD	GKICTVTGWG	NTQYYGQQ.A	GVLQEAAPVI	ISNDVCNGAD
Tadg15	SMVRPICLPD	...ASHVFPA	GKAIWVTGWG	HTQYGGTG.A	LILQKEIRV	INQTTCE..N
Scce	SMVKKVRLPS	...RCE..PP	GTTCTVSGWG	TTTSPDVTFP	SDLMCVDVKL	ISPQDCTKV.
Try	ARVSTISLPT	...APP..AT	GTKCLISGWG	NTASSGADYP	DELQCLDAPV	LSQAKCEAS.
Chymb	QTVSAVCLPS	...ADDDFPA	GTLCATGWG	KTKYNANKTP	DKLQQAALPL	LSNAECKKS.
Fac7	DHVVPLCLPE	RTFSERTLAF	VRFSLVSGWG	QLLDRGATAL	ELMVLNVPRL	NTQDCLQQSR
Tpa	QESSVVRTVC	LPPADLQLPD	WTECELSGYG	KHEALSPFYS	ERLKEAHVRL	YPSSRCTSQH

Fig. 1A

\*

Heps	FYGN..QIKP	KMFCAGYPEG	G.....IDA	CQDSDGGPFV	CEDSISRTPR	WRLCGIVSWG
Tadg15	LLPQ..QITP	RMMC VGFLSG	G.....VDS	CQDSDGGPL.	..SSVEADGR	IFQAGVVSWG
Scce	.YKD..LLEN	SMLCAGIPDS	K.....KNA	CNGDSDGGPLV	C....R....	GTLQGLVSWG
Try	.YPG..KITS	NMFCVGFLSG	G.....KDS	CQDSDGGPVV	C....M....	GQLQGVVSWG
Chymb	.WGR..RITD	VMICAG..AS	G.....VSS	CMGDSDGGPLV	C....QKDG	WTLVGIVSWG
Fac7	KVGDSPNITE	YMFCAGYS DG	S.....KDS	CKGDSDGGP..	..HATHYRGT	WYLTGIVSWG
Tpa	LLNRT..VTD	NMLCAGDTRS	GGPQANLHDA	CQDSDGGPLV	CLN....DGR	MTLVGIISWG
Heps	T.GCALAQKP	GVYTKVSDFR	EWIFQAIKTH	SEASGXVTQL	--	(SEQ ID NO: 3)
Tadg15	D.GCAQRNKP	GVYTRLP LFR	DWIKENTGV-	-----	--	(SEQ ID NO: 14)
Scce	TFPCGQPN DP	GVYTQVCKFT	KWINDTMKKH	R-----	--	(SEQ ID NO: 4)
Try	D.GCAQKNKP	GVYTKVYNYV	KWIKNTIAAN	S-----	--	(SEQ ID NO: 5)
Chymb	DSTCS.TSSP	GVYARVTCLI	PWVQKILAA N	-----	--	(SEQ ID NO: 6)
Fac7	Q.GCATVGHF	GVYTRVSQYI	EWLQKLMRSE	PRPGVLLRAP	FP	(SEQ ID NO: 7)
Tpa	.LGGGQKDVP	GVYTKVTNYL	DWIRDNMRP-	-----	--	(SEQ ID NO: 8)

Fig. 1B

1 TCAAGAGCGCCTCGGGGTACCATGGGAGCGATCGGGCCCGCAAGGGCGGAGGGGCCCGAAGGACTTCGGCGC  
M G S D R A R K G G G P K D F G A 18  
76 GGGACTCAAGTACAACCTCCGGCAGAGAAAGTGAATGGCTTGGAGGAAGCGTGGAGTTCTCTGCCAGTCAACAA  
G L K Y N S R H E K V N G L E E G V E F L P V N N 43  
151 CGTCAAGAAGGTGGAAGCATGGCCCGGGCGCTGGGTGGTGGCAGCCGTGCTGATCGGCCCTCCTCTTGGT  
V K K V E K H G P G R W V V L A A V L I G L L L V 68  
226 CTTCGCTGGGATCGGCTTCCTGGTGTGGCATTTGCAGTACCGGACGTGCGTGTCCAGAAAGTCTTCAATGGCTA  
L L G I G F L V W H L Q Y R D V R V Q K V F N G Y 93  
301 CATGAGGATCACAAATGAGAAATTTGTGGATGCCTACGAGAACTCCAACCTCCACTGAGTTTGTAAAGCCTGGCCAG  
M R I T N E N F V D A Y E N S N S T E F V S L A S 118  
376 CAAGTGAAGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTGGGCCCCCTACCACAAGGAGTCGGCTGT  
K V K D A L K L L Y S G V P F L G P Y H K E S A V 143  
451 GACGGCCTTCAGCGAGGCGCGTCATCGCCTACTACTGGTCTGAGTTTCAGCATCCCGCAGCACCTGGTGGAGGA  
T A F S E G S V I A Y Y W S E F S I P Q H L V E E 168  
526 GCGCGAGCGCTCATGGCCGAGGAGCGCGTAGTCATGCTGCCCCCGGGCGCGCTCCCTGAAGTCCTTTGTGGT  
A E R V M A E E R V V M L P P R A R S L K S F V V 193  
601 CACCTCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAAACAGCTGCAGCTTTGGCCT  
T S V V A F P T D S K T V Q R T Q D N S C S F G L 218  
676 GCACGCCCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCTGACAGCCCCCTACCCCGCTCATGCCCG  
H A R G V E L M R G T T P G R P D S P Y P A H A R 243

Fig. 2A


751 CTGCCAGTGGGCCCTGCGGGGACGCCGACTCAGTGTCTGAGCCTCACCTTCCGCAGCTTTGACCTTGCCTCCTG  
C Q W A L R G D A D S V L S L T F R S F D L A S C 268  
826 CGACGAGCGCGCAGCAGCTGGTGACGGGTGTACAACACCCCTGAGCCCCATGGAGCCCCACGCCCTGGTGCACTT  
D E R G S D L V T V Y N T L S P M E P H A L V Q L 293  
901 GTGTGGCACCTACCTCCCTCCTACAACCTGACCTTCCACTCTCCAGAACGTCTCTGCTCATCACACTGATAAC  
C G T Y P P S Y N L T F H S S Q N V L L I T L I T 318  
976 CAACACTGAGCGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTGCCCTAGGATGAGCAGCTGTGGAGGCCG  
N T E F F H P G F E A T F F Q L P R M S S C G G R 343  
1051 CTTACGTAAAGCCAGGGACATTCAACAGCCCCCTACTACCCAGGCCACTACCCACCAACATTGACTGCACATG  
L R K A Q G T F N S P Y Y P G H Y P P N I D C T W 368  
1126 GAACATTGAGGTGCCCAACCAAGCATGTGAAGTGAGCTTCAAATTCTTCTACCTGTGGAGCCCCGGCGTGCC  
N I E V P N N Q H V K V S F K F Y L L E P G V P 393  
1201 TCGGGCACCTGCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCCCAGTTTCGTCGT  
A G T C P K D Y V E I N G E K Y C G E R S Q F V V 418  
1276 CACCAGCAACAGCAAGATCACAGTTTCGCTTCCACTCAGATCAGTCCACCCGACACCGGCTTCTTAGCTGA  
T S N S N K I T V R F H S D Q S Y T D T G F L A E 443  
1351 ATACCTCTCCTACGACTCCAGTGACCCCATGCCCGGGCAGTTACGTGCCCGCACGGGGCGGTGTATCCGGAAGGA  
Y L S Y D S S D P C P G Q F T C R T G R C I R K E 468  
1426 GCTGCGCTGTGATGGCTGGGCCGACTGCACCCGACACAGCGATGAGCTCAACTGCAGTTCGACGCGCGCCACCA  
L R C D G W A D C T D H S D E L N C S C D A G H Q 493

**Fig. 2B**

1501 GTTACAGTGAAGAACAAGTTCTGTCAAGCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGCGGAGACAACAG 518  
F T C K N K F C K P L F W V C D S V N D C G D N S  
1576 CGACGAGCAGGGTGCAGTTGTCCGGCCACAGACCTTCAGGTGTTCCAATGGGAAGTGCCCTCTCGAAAAGCCAGCA 543  
D E Q G C S C P A Q T F R C S N G K C L S K S Q Q  
1651 GTGCAATGGGAAGGACGACTGTGGGACGGGTCCGACGAGCCCTCCTGCCCCAAGGTGAACGTCGTCACTTGTAC 568  
C N G K D D C G D G S D E A S C P K V N V T C T  
1726 CAAACACACCTACCGCTGCCCTCAATGGGCTCTGCTTGAGCAAGGCAACCCCTGAGTGTGACGGGAAGGAGGACTG 593  
K H T Y R C L N G L C L S K G N P E C D G K E D C  
1801 TAGCGACGGCTCAGATGAGAAAGGACTGCGACTGTGGGCTGCGGTCAATTCACGAGACAGGCTCGTGTGTGGGG 618  
S D G S D E K D C D C G L R S F T R Q A R V V G G  
1876 CACGGATCGGATGAGGGCGAGTGGCCCTGGCAGGTAAAGCCTGCATGCTCTGGGCCAGGGCCACATCTGCGGTGC 643  
T D A D E G E W P W Q V S L H A L G Q G H I C G A  
1951 TTCCCTCATCTCTCCAACTGGCTGGTCTCTGCCGACACTGCTACATCGATGACAGAGGATTCAGTACTCAGA 668  
S L I S P N W L V S A A (H) C Y I D D R G F R Y S D  
2026 CCCCACGAGTGGACGGCCTTCCCTGGGCTTGACACGACCAGAGCCAGCGCCCTGGGTGCAGGAGCGCAG 693  
P T Q W T A F L G L H D Q S Q R S A P G V Q E R R  
2101 GCTCAAGGCATCATCTCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTGCTGGAGCTGGA 718  
L K R I I S H P F F N D F T F D Y (D) I A L L E L E  
2176 GAAACCGGCAGATACAGCTCCATGTTGCGGCCCATCTGCCGTGGACGCCCTCCCATGTCTTCCCTGCCGGCAA 743  
K P A E Y S S M V R P I C L P D A S H V F P A G K

Fig. 2C

2251 GGCCATCTGGGTCACGGGCTGGGGACACACCCAGTATGGAGGCACCTGGCGCGCTGATCCTGCAAAAAGGGTGAGAT  
 A I W V T G W G H T Q Y G G T G A L I L Q K G E I 768  
 2326 CCGCGTCATCAACAGACCACTGCGAGAACCTCCTGCCGAGCAGATCACGCCGCGCATGATGTGCGTGGGCTT  
 R V I N Q T T C E N L L P Q Q I T P R M C V G F 793  
 2401 CCTCAGCGCGGCGTGGACTCCTGCCAGGTGATTCGGGGGACCCCTGTCCAGCGTGGAGGCGGATGGGCGGAT  
 L S G G V D S C Q G D (S) G G P L S S V E A D G R I 818  
 2476 CTTCCAGGCCGGTGTGGTGAAGCTGGGAGACGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACAAAGGCTCCC  
 F Q A F C C S W G D G C A Q R N K P G V Y T R L P 843  
 2551 TCTGTTTCGGGACTGGATCAAAGAGAACACTGGGGTATAGGGCGCGGCCACCCAAATGTGTACACCTGCCGGG  
 L F R D W I K E N T G V (SEQ ID NO: 2) 855  
 2626 CCACCCATCGTCCACCCAGTGTGCACGCCCTGCAGGCTGGAGACTGGACCCGCTGACTGCACCCAGCGCCCCAGAA  
 2701 CATACTGTGAACCTCAATCTCCAGGCTCCAAATCTGCCTAGAAAACCTCTCGCTTCCTCAGCCTCCAAAGTGG  
 2776 AGCTGGGAGGTAGAAAGGGAGGACACTGGTGGTTCTACTGACCCAACTGGGGGCAAGGTTTGAAGACACAGCCT  
 2851 CCCCCGCCAGCCCCAAGCTGGGCCGAGGCGCGTTTGTGTATATCTGCCCTCCCTGTCTGTAGGAGCAGCGGAA  
 2926 CGGAGCTTCGGAGCCTCCTCAGTGAAGGTGGTGGGCTGCCGATCTGGGCTGTGGGCCCTTGGGCCACGCTCT  
 3001 TGAGGAAGCCAGGCTCGGAGGACCCCTGGAACACAGACGGTCTGAGACTGAAATGTATTACAGCTCCCAGGG  
 3076 TGGACTTCAGTGTGTATTGTGTAATGGGTAAACAATTATTCTTTTAAAAAATAAAAAA  
 (SEQ ID NO: 1)

 : KOZAK'S CONSENSUS SEQUENCE

 : TRANSMEMBRANE DOMAIN


 : CONSERVED AMINO ACIDS OF CATALYTIC TRIAD H,D,S

Fig. 2D

1 MGSDRARKGG GGPKEFGAGL KYNSRHEKVN GLEEGVEFLP VNNVKKVEKH 1  
 51 GPGRWVVLAA VLI GLLLVL GIGFLVWHLQ YRDVRVQKVF NGYMRITNEN 2  
 101 FVDAYENSNS TEFVSLASKV KDALKLLYSG VPFLGPYHKE SAVTAFSEGS  
 151 VIAYYWSEFS IPQHLVEEAE RVMAEERVVM LPPRARSLSK FVVTSVVAF P  
 201 TDSKTVQRTQ DNS\*CSFGLHA RGVELMRFTT PGFPDSPYPA HARCQWALRG  
 251 DADSVLSLTF RSFDLAS\* CDE RGSDLVTVYN T LSPMEPHAL VQL\*CGTYPPS  
 301 YNLT FHSSQN VLLITLITNT ERRHPGF EAT FFQLPRMSSC\* GGRLRKAQGT 3  
 351 FNSPYYPGHY PPNID\* CTWNI EV PNNQHVKV SFKFFYLLEP GVPAGT\*CPKD  
 401 YVEINGEKYC\* GERSQFV VTS NSNKITVRFH SDQSYTDTGF LAEYLSYDSS  
 451 DPCPGQFTCR TGR CIRKELR CDGWADCTDH SDE LNCSCDA GHQFTCKNKF  
 501 CKPLFWVCDS VND CGDN SDE QGCSCPAQTF RCSNGKCLSK SQQCNGKDDC 4  
 551 GDG SDE ASCP KVN VVTCTKH TYRCLNGLCL SKGNPECDGK EDCSDG SDEK  
 601 DCDCGLRSFT RQARV VGGTD ADEGEWPWQV SLHALGQGHI CGASLISP NW  
 651 LVSAAH CYID DRGFRYSDPT QWTAFLGLHD QSQRSAPGVQ ERRLKRIISH  
 701 PPFNDFTFDY DIALLELEKP AEYSSMVRPI CLPDASHVFP AGKAIWVTGW 5  
 751 GHTQYGGTGA LILQGEIRV INQTT CENLL PQQITPRMMC VGFLSGGVDS  
 801 CQGD SGGPLS SVEADGRIFQ AGVVS WGDGC AQRNKPGVYT RLPLFRDWIK  
 851 ENTGV (SEQ. ID NO: 2)

\* : Conserved cysteine residue

NXT : Possible N-linked glycosylation site

SDE : Conserved SDE motif

▼ : Potential cleavage site

O : Conserved amino acids of catalytic triad H, D, S

1. Cytoplasmic domain

2. Transmembrane domain

3. CUB repeat

4. Ligand-binding repeat (class A motif)  
of LDL receptor like domain

5. Serine protease

Fig. 3

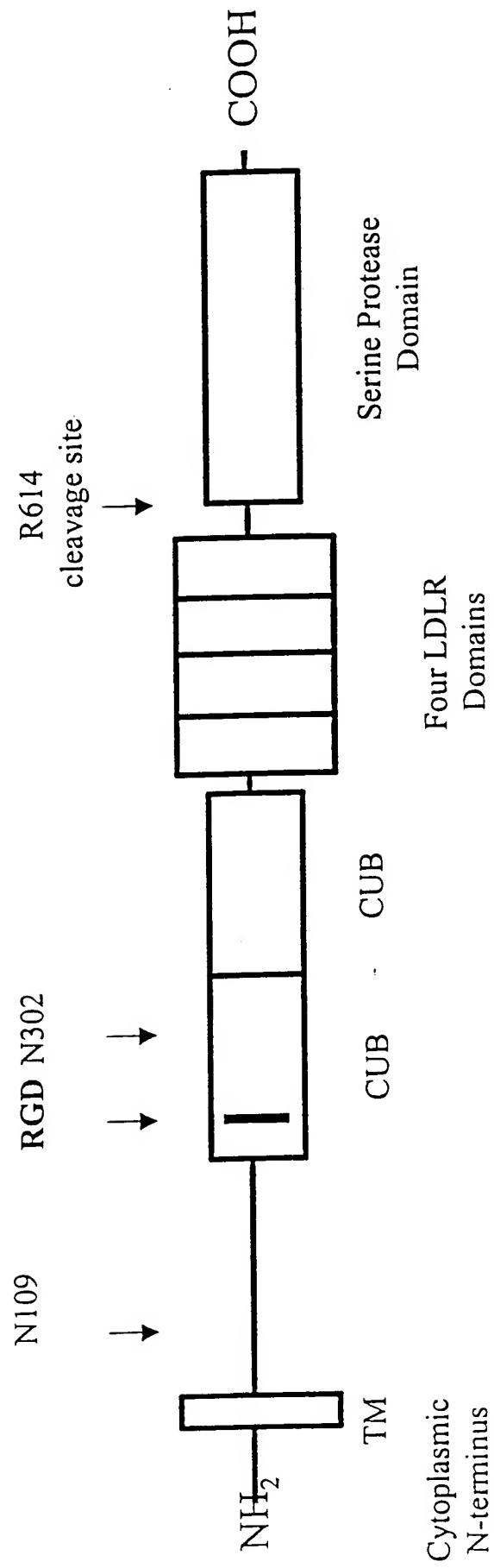


Fig. 4



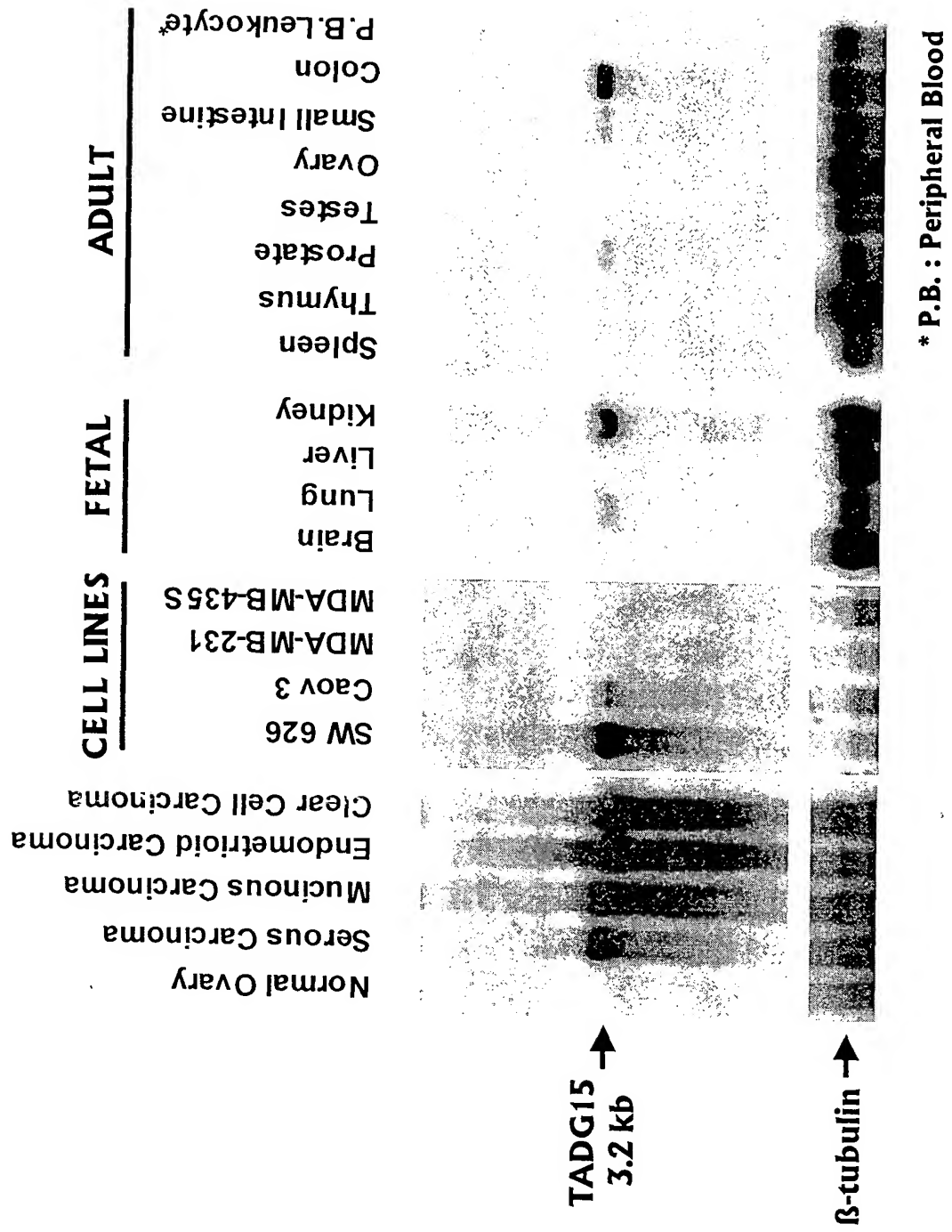


Fig. 5

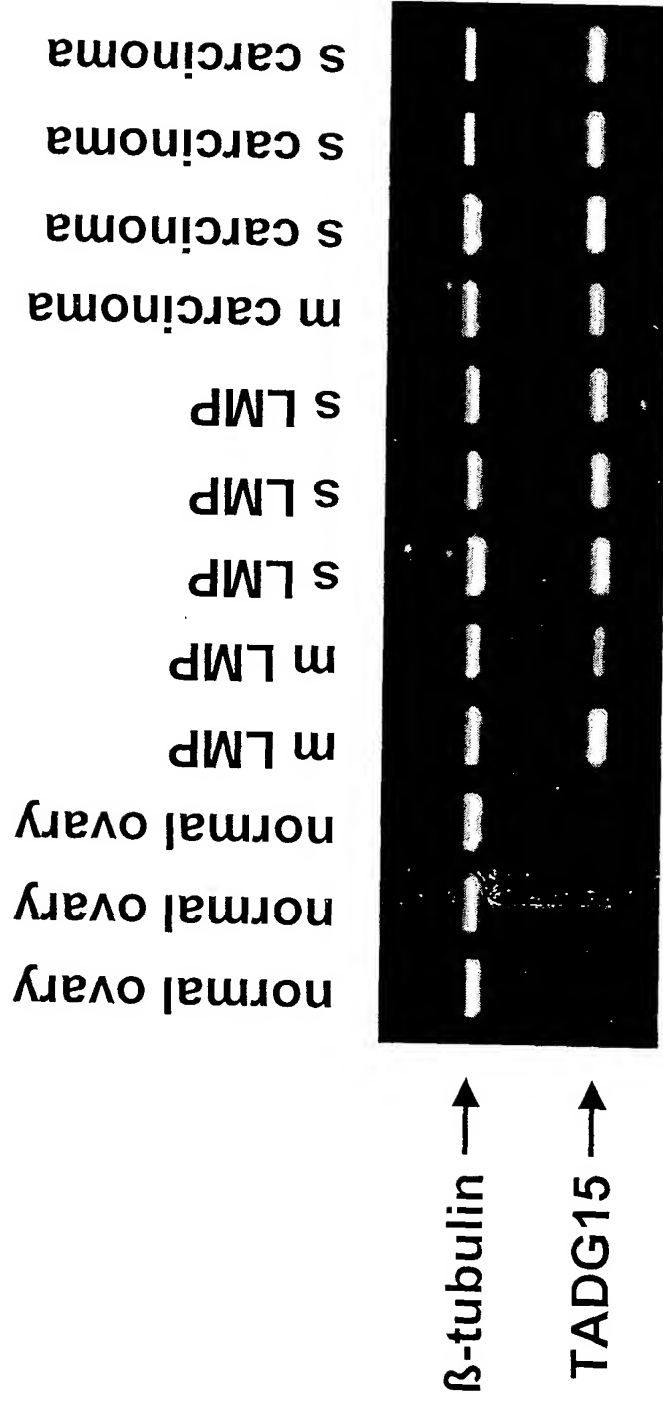
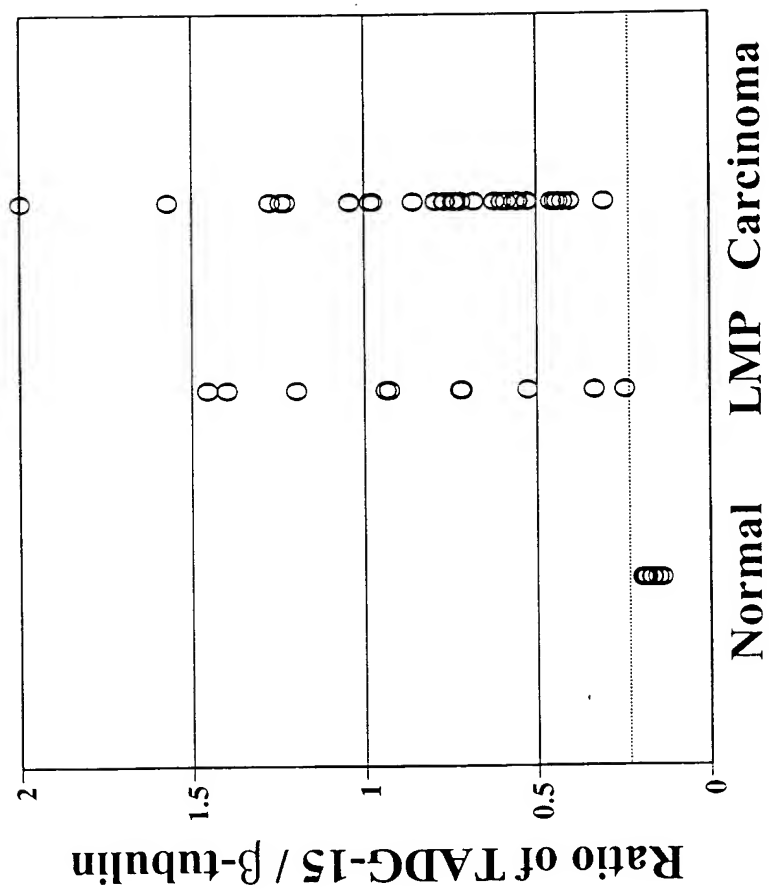


Fig. 6A



**Fig. 6B**

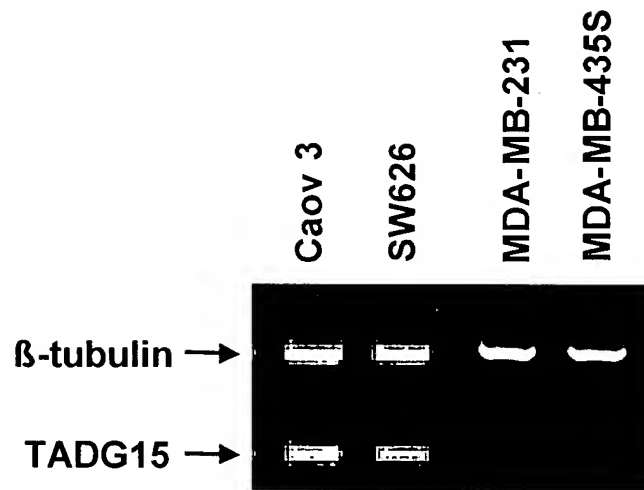


Fig. 7

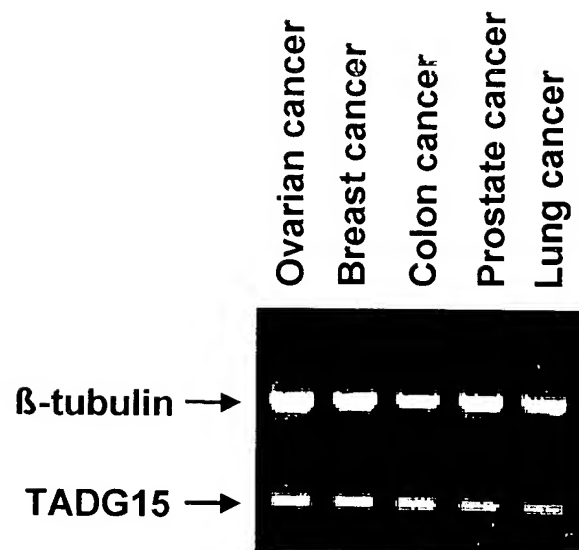


Fig. 8

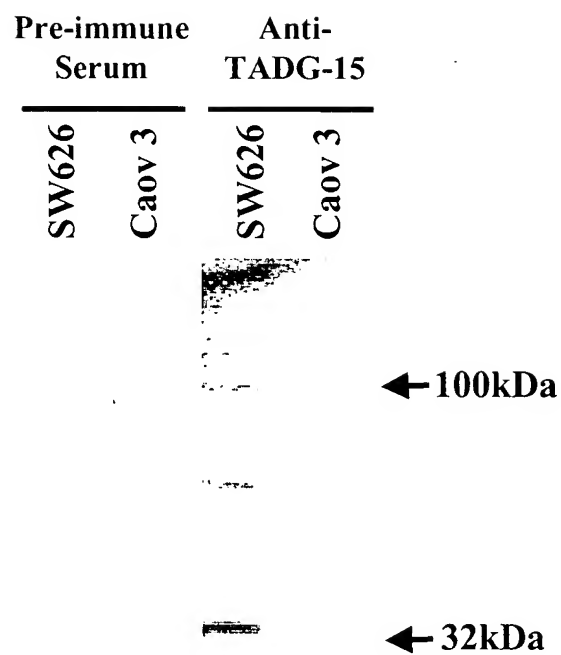


Fig. 9



Fig. 10A



Fig. 10B

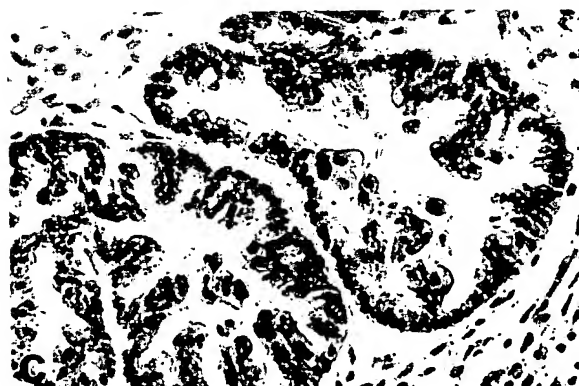


Fig. 10C

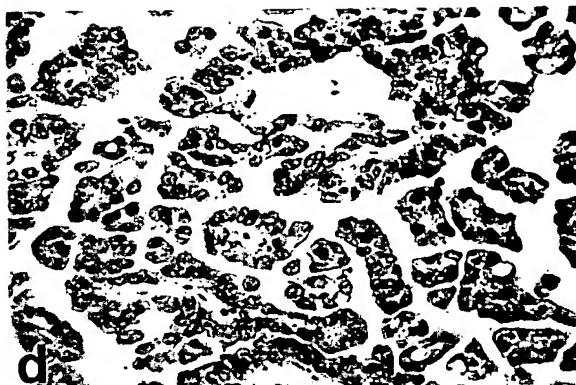


Fig. 10D



Fig. 10E

hTADG15	MGSDRARKGG	GGPKDFGAGL	KYNSRHEKVN	GLEEGVEFLP	VNNVKKVERH	50
mEpithin	---N-G--A-	--SQ-----	--D--L-NM-	-F-----	A--A-----R	
hTADG15	GPGRWVVLAA	VLIGLLLVLL	GIGFLVHLQ	YRDVRVQKVF	NGYMRITNEN	100
mEpithin	--R-----V-	--FSF--LS-	MA-L----FH	--N-----	--HL-----I	
hTADG15	FVDAYENSNS	TEFVSLASKV	KDALKLLYSG	VPFLGPYHKE	SAVTAASEGS	150
mEpithin	-L-----T-	---I-----Q-	-E-----NE	--V-----K	-----	
hTADG15	VIAYWSEFS	IPQHLVEEAE	RVMAEERVVM	LPPRARSILKS	FVVTSVVAFF	200
mEpithin	-----	--P--A--VD	-A--V----T	-----A---	--L-----	
hTADG15	TDSKTVQRTQ	DNSCSFGLHA	RGVELMRFTT	PGFPDSPYPA	HARCQWALRG	250
mEpithin	I-PRML----	-----A----	H-AAVT----	-----N----	-----V----	
hTADG15	DADSVLSLTF	RSEDLASCDE	RGSDLVTVYN	TLSPMEPHAL	VQLCGTYPPS	300
mEpithin	-----	---V-P---	H-----D	S-----V	-R-----FS--	
hTADG15	YNLTFHSSQN	VLLITLITNT	ERRHPGFEAT	FFQLPRMSSC	GGRLRKAQGT	350
mEpithin	-----L----	-F-V-----	G--L-----	-----K----	--V-SDT----	
hTADG15	FNSPYPGPHY	PPNIDCTWNI	EVPNNQHVKV	SEKFFYLLEP	GVPAGTCPKD	400
mEpithin	-S-----	---N-----	K-----RN---	R--L---VD-	N--V-S-T--	
hTADG15	YVEINGEKYC	GERSQFVVTS	NSNKITVRFH	SDQSYTDGTF	LAEYLSYDSS	450
mEpithin	-----GS	-----S-	--S-----H--	--H-----	-----N	

Fig. 11A



hTADG15	DPCPGQFTCR	TGRCIRKELR	CDGWADCTDH	SDELNCSCDA	GHQFTCKNKF	500
mEpithin	-----M-M-K	-----	-----P-Y	---RY-R-N-	T-----Q-	
hTADG15	CKPLFWVCDs	VNDCGDnsDE	QGCsCPAQTF	RCSNGKCLSK	SQQCNGKDDC	550
mEpithin	-----	-----G---	E-----GS-	K-----PQ	--K-----N-	
hTADG15	GDGSDEAsCP	KVNvVTCTKH	TYRCLNGlCL	SKGNPECDGK	EDCSDGSDEK	600
mEpithin	-----D	S---S---Y	-----Q---	-----	T-----	
hTADG15	DCDCGLRsFT	RQARvVGgTD	ADEGEwPwQV	SLHALGQGHl	CGASLIspNW	650
mEpithin	N-----	K-----N	-----	-----L	-----D-	
hTADG15	LVsAAHCYID	DRGERYSDEPT	QWTAFLGLHD	QsQRsAPGVQ	ERRLKRIISH	700
mEpithin	-----FQ-	-KN-K---Y-	M-----L-	--K---S---	-LK-----T-	
hTADG15	PFFNDFTFDY	DIALLELEKP	AEYSSMVRPI	CLPDASHVFP	AGKAIWVTGW	750
mEpithin	-S-----	-----S	V---TV---	-----T---	-----	
hTADG15	GHTQYGGTGA	LILQKGEIRV	INQTTcENLL	PQQITPRMMC	VGFLSGGVDS	800
mEpithin	---KE-----	-----	-----D-M	-----	-----	
hTADG15	CQGDsGGPLs	SVEADGRIFQ	AGVVSWGdGC	AQRNKPGVYT	RLPLFRDWIK	850
mEpithin	-----	-A-K---M-	-----E-	-----	---CSSGLDQ	
hTADG15	ENTGV*					900
mEpithin	RAHWGIAAwT	DSRPQTPTGM	PDMHTWIOER	NTDDIYAVAS	PPQHNPDCEL	
hTADG15		SEQ ID NO: 2				902
mEpithin	HP	SEQ ID NO: 10				

TADG15: TCAAGAGCGGCCTCGGGGTACCAATGGGAGCGCATCGGGCCCGCAAGGGCGGAGGGGCCCGAAGGACTTCGGCGCGGGACT 81

SNC19: .....  
.....  
.....

82 CAAGTACAACCTCCCGCAGAGAAAGTGAAATGGCTTGGAGGAGCGGTGGAGTTCTTGCCAGTCAACAACGTCAAGAGGTGGAAAAAGCATGGCCCGGGG  
.....  
.....

182 CGCTGGGTGGTGTGGCAGCCGTTGCTGATCGGCCCTCCTCTTGGTCTTGTTTGGGGATCGGCTTCCCTGGTGTGGCATTTTCAGATACCGGGACGTGCGTGTCC 281  
|||||  
1 CGCTGGGTGGTGTGGCAGCCGTTGCTGATCGGCCCTCCTCTTGGTCTTGTCTGGGGATCGGCTTCCCTGGTGTGGCATTTTCAGATACCGGGACGTGCGTGTCC 100  
|||||

282 AGAAGGTCTTCAATGGCTACATGAGGATCACAAATGAGAAATTTGTGGATGCCCTACGAGAACTCCAACCTCCACTGAGTTGTAAAGCCTGGCCAGCAAGGT 381  
|||||

101 AGAAGGTCTTCAATGGCTACATGAGGATCACAAATGAGAAATTTGTGGATGCCCTACGAGAACTCCAACCTCCACTGAGTTGTAAAGCCTGGCCAGCAAGGT 200  
|||||

382 GAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCTCGGGCCCCCTACCACAAGGAGTCGGCTGTGACGSCCTTCAGCGAGGGCAGCGTCATCGCC 481  
|||||

201 GAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCTCGGGCCCCCTACCACAAGGAGTCGGCTGTGACGSCCTTCAGCGAGGGCAGCGTCATCGCC 300  
|||||

482 TACTACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGAGGCCGAGCGGTCAATGGCCGAGGAGCGGTAGTCATGCTGCCCCCGGGCGCGCT 581  
|||||

301 TACTACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGTGGAGAGGCCGAGCGGTCAATGGCC .AGGAGCGGTAGTCATGCTGCCCCCGGGCGCGCT 399  
|||||

582 CCCTGAAGTCCCTTGTGGTCAACCTCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGACCACCCAGGACAAACAGCTGCAGCTTTGGCCTGCACGC 681  
|||||

400 CCCTGAAGTCCCTTGTGGTCAACCTCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAAACAGCTGCAGCTTTGGCCTGCACG . 498  
|||||

Fig. 12A

682 CCGCGGTGTGGAGCTGATGCGCTTCACACGCCCGGCTTCCCTGACAGCCCCCTACCCCGCTCATGCCCCGTGCCAGTGGGCCCTGCGGGGGACGCCGAC 781  
|||||  
499 CCGCGGTGTGGAGCTGATGCGCTTCACACAG.CCGGCTTCCCTGACAGCCCCCTACCCCGCTCATGCCCCGTGCCAGTGGGT...TGCGGGGACG.CGAC 592  
|||||  
782 TCAGTGCTGAGCCTCACCTTC....CGCAGCTTTGACCTTGCGTCCCTGCGACGCGCGCAGCAGCCTGGTGACGGTGTACAACACACCCCTGAGCCCCCAT 876  
|||||  
593 GCAGTGCTGAGCTACTCGAGCTGACTCGCAGC.TTGACTGCGCCT...CGACGAGCGCGGCAGCAGCCTGGTGAC.GTGTAACAACACCCCTGAGCCCCCAT 686  
|||||  
877 GGAGCCCCACGCCCTGGTGCAGTTGTGTGGCACCTACCCCTCCCTCCTACAACCTGACCTTCCACT.CCTCCCA.GAACGTCCTGCTCATCACACTGATAA 974  
|||||  
687 GGAGCCCCACG.CCTGCTG...AGTGTGTGGCACCTACCCCTCCCTCCTACAACCTGACCTTCCACTCCCTCCCAAGAACGTCCTGCTCATCACACTGATAA 783  
|||||  
975 CCAACACTGAGCGGGCGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTGCGCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCAGGGGACATT 1074  
|||||  
784 CCAACACTGA..CGCGGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTGCGCTAGGATGAGCAGCTGTGGAGGCCGCTTACGTAAAGCCAGGGGACATT 881  
|||||  
1075 CAACAGCCCCCTACTACCCAGGCCCACTACCCACCCCAACATTGACTGCACATGGAACATTGAGGTGCCCAACAACCAGCATGTGAAGGTGAGCTTCAAATTC 1174  
|||||  
882 CAACAGCCCCCTACTACCCAGGCCCACTACCCACCCCAACATTGACTGCACATGGAACATTGAGGTGCCCAACAACCAGCATGTGAAGGTGCGCTTCAAATTC 981  
|||||  
1175 TTCTACCTGCTGGAGCCCGCGGTGCCCTGCGGGCACCTGCCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCCCAGTTCGTCG 1274  
|||||  
982 TTCTACCTGCTGGAGCCCGCGGTGCCCTGCGGGCACCTGCCCCCAAGGACTACGTGGAGATCAATGGGGAGAAATACTGCGGAGAGAGGTCCCAGTTCGTCG 1081  
|||||  
1275 TCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCCCTACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGA 1374  
|||||  
1082 TCACCAGCAACAGCAACAAGATCACAGTTCGCTTCCACTCAGATCAGTCCCTACACCGACACCGGCTTCTTAGCTGAATACCTCTCCTACGACTCCAGTGA 1181  
|||||

**Fig. 12B**

1375 CCCATGCCCGGCGAGTTACGTGCCCCGACAGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGGGCCGACTGCACCGACCACAGCGATGAGCTC 1474  
|||||  
1182 CCCATGCCCGGCGAGTTACGTGCCCCGACAGGGGCGGTGTATCCGGAAGGAGCTGCGCTGTGATGGCTGGG.CGACTGCACCGACCACAGCGATGAGCTC 1290  
|||||  
1475 AACTGCAGTTGCGACGCCGGCCACCAGTTTCAAGTTCGCAAGAAACAAGTTCTGCAAGCCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGCGGAGACAACA 1574  
|||||  
1281 AACTGCAGTTGCGACGCCGGCCACCAGTTTCAAGTTCGCAAGAAACAAGTTCTGCAAG...CTCTTCTGGGTCTGCGACAGTGTGAACGAGTGTGCGGAGACAACA 1377  
|||||  
1575 GCGACGAGCAGGGGTGCAAGTTGTCCGG.CCCAGACCTTTCAGGTGTTCCAAATGGGAAGTGCCCTCTCGAAAAGCCAGCAGTGCATGCGGAAGGACGACTGTG 1673  
|||||  
1378 GCGACGAGCAGGGGTGCAATTTGTCCGGACCCAGACCTTTCAGGTGTTCCAAATGGGAAGTGCCCTCTCGAAAAGCCAGCAGTGCATGCGGAAGGACGACTGTG 1477  
|||||  
1674 GGGACGGGTCCGACGAGGCCCTCCTGCCCCCAAGGTGAACGTGTCACTTGTACCAAAACACACCTACCCTGCCCTCAATGGGCTCTGCTTGAGCAAGGGCAA 1773  
|||||  
1478 GGGACGGGTCCGACGAGGCCCTCCTGCCCCCAAGGTGAACGTGTCACTTGTACCAAAACACACCTACCCTGCCCTCAATGGGCTCTGCTTGAGCAAGGGCAA 1577  
|||||  
1774 CCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAGGACTGCGACTGTGGGTGCGGTTCATTACGAGACAGGCTCGTGTGTTGGG 1873  
|||||  
1578 CCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAGGACTGCGACTGTGGGTGCGGTTCATTACGAGACAGGCTCGTGTGTTGGG 1677  
|||||  
1874 GGCACGGATGCGGATGAGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCTGTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGC 1973  
|||||  
1678 GGCACGGATGCGGATGAGGCGAGTGGCCCTGGCAGGTAAGCCTGCATGCTGTGGGCCAGGGCCACATCTGCGGTGCTTCCCTCATCTCTCCCAACTGGC 1777  
|||||  
1974 TGGTCTCTGCCCCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCCACGAGTGGACGGCCTTCCCTGGGCTTGCACGACCAGAGCCAGCG 2073  
|||||  
1778 TGGTCTCTGCCCCACACTGCTACATCGATGACAGAGGATTCAGGTACTCAGACCCCCACGCA..GGACGGCCTTCCCTGGGCTTGCACGACCAGAGCCAGCG 1875

Fig. 12C

2074 CAGCGCCCTGGGGTGCAGGAGCGCAGGCTCAAGCGCATCATCTCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTGCTGGAGCTG 2173

1876 CA..GGCCCTGGGGTGCAGGAGCGCAGGCTCAAGCGCATCATCTCCACCCCTTCTTCAATGACTTCACCTTCGACTATGACATCGCGCTGCTGGAGCTG 1973

2174 GAGAAACCGGCAGAGTACAGCTCCATGGTGGGCCCATCTGCCCTGCCGACGCCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTACCGGCTGGG 2273

1974 GAGAAACCGGCAGAGTACAGCTCCATGGTGGGCCCATCTGCCCTGCCGACGCCCTCCCATGTCTTCCCTGCCGGCAAGGCCATCTGGGTACCGGCTGGG 2073

2274 GACACACCCAGTATGGAGGCACCTGGCGCGCTGATCCTGCAAAAGGCTGAGATCCGCGTCAATCAACCAGACACCCTGCGAGAACCTCTCTGCCCGCAGCAGAT 2373

2074 GACACACCCAGTATGGAGGCACCTGGCGCGCTGATCCTGCAAAAGGCTGAGATCCGCGTCAATCAACCAGACACCCTGCGAGAACCTCTCTGCCCGCAGCAGAT 2173

2374 CACGCCCGCATGATGTGCGTGGGCTTCCTCAGCGGGCGGTGACTCCTGCCAGGGTGATTCGGGGGACCCCTGTCTCCAGCGTGGAGCGGATGGGCGG 2473

2174 CACGCCCGCATGATGTGCGTGGGCTTCCTCAGCGGGCGGTGACTCCTGCCAGGGTGATTCGGGGGACCCCTGTCTCCAGCGTGGAGCGGATGGGCGG 2273

2474 ATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGCTGCGCTCAGAGGAACAAGCCAGGCGGTATACACAAGGCTCCCTCTGTTTCGGGACTGGATCAAAG 2573

2274 ATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGAC . GCTGCGCTCAGAGGAACAAGCCAGGCGGTATACACAAGGCTCCCTCTGTTTCGGGAATGGATCAAAG 2372

2574 AGAACACTGGGGTATAGGGCCCGGGGCCACCCAAATGTGTACACCTGCGGGGCCACCCCATCGTCCACCCCAAGTGTGCACGCTGCAGGCTGGAGACT... 2670

2373 AGAACACTGGGGTATAGGGCCCGGGGCCACCCAAATGTGTACACCTGCGGGGCCACCCCATCGTCCACCCCAAGTGTGCACGCTGCAGGCTGGAGACTCGC 2472

2671 GGACCGCTGACTGCACCAAGCGCCCCCAGAAACATACACTGTGAACCTCAATCTCCAGGGCTCCAAATCTGCCTTAGAAAAACCTCTCGCTTCCTCAGCCTCCAA 2770

2473 GCACCGTGACCTGCACCAGCG . CCCCAGAACATACACTGTGAACCTC . ATCTCCAGG . . CTCAAATCTG . CTAGAAAAACCTCTCGCTTCCTCAGCCTCCAA 2567

**Fig. 12D**

[illegible]

**Fig. 12E**